



09/587574

SEQUENCE LISTING

<110> Max-Delbrück-Centrum für Molekulare Medizin

<120> Conductine protein and a related agent for diagnosing
and treating tumor illnesses

<130> 0107-026 US

<140> 09/587,574

<141> 2000-06-05

<150> DE 197 38 205.3

<151> 1997-09-02

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conductine
protein

<400> 1

Met Ser Ser Ala Val Leu Val Thr Leu Leu Pro Asp Pro Ser Ser Ser
1 5 10 15

Phe Arg Glu Asp Ala Pro Arg Pro Pro Val Pro Gly Glu Glu Gly Glu
20 25 30

Thr Pro Pro Cys Gln Pro Ser Val Gly Lys Val Gln Ser Thr Lys Pro
35 40 45

Met Pro Val Ser Ser Asn Ala Arg Arg Asn Glu Asp Gly Leu Gly Glu
50 55 60

Pro Glu Gly Arg Ala Ser Pro Asp Ser Pro Leu Thr Arg Trp Thr Lys
65 70 75 80

Ser Leu His Ser Leu Leu Gly Asp Gln Asp Gly Ala Tyr Leu Phe Arg
85 90 95

Thr Phe Leu Glu Arg Glu Lys Cys Val Asp Thr Leu Asp Phe Trp Phe

100					105					110						
Ala	Cys	Asn	Gly	Phe	Arg	Gln	Met	Asn	Leu	Lys	Asp	Thr	Lys	Thr	Leu	
115					120					125						
Arg	Val	Ala	Lys	Ala	Ile	Tyr	Lys	Arg	Tyr	Ile	Glu	Asn	Asn	Ser	Val	
130					135					140						
Val	Ser	Lys	Gln	Leu	Lys	Pro	Ala	Thr	Lys	Thr	Tyr	Ile	Arg	Asp	Gly	
145					150					155					160	
Ile	Lys	Lys	Gln	Gln	Ile	Gly	Ser	Val	Met	Phe	Asp	Gln	Ala	Gln	Thr	
165					170					175						
Glu	Ile	Gln	Ala	Val	Met	Glu	Glu	Asn	Ala	Tyr	Gln	Val	Phe	Leu	Thr	
180					185					190						
Ser	Asp	Ile	Tyr	Leu	Glu	Tyr	Val	Arg	Ser	Gly	Gly	Glu	Asn	Thr	Ala	
195					200					205						
Tyr	Met	Ser	Asn	Gly	Gly	Leu	Gly	Ser	Leu	Lys	Val	Leu	Cys	Gly	Tyr	
210					215					220						
Leu	Pro	Thr	Leu	Asn	Glu	Glu	Glu	Glu	Trp	Thr	Cys	Ala	Asp	Leu	Lys	
225					230					235					240	
Cys	Lys	Leu	Ser	Pro	Thr	Val	Val	Gly	Leu	Ser	Ser	Lys	Thr	Leu	Arg	
245					250					255						
Ala	Thr	Ala	Ser	Val	Arg	Ser	Thr	Glu	Thr	Ala	Glu	Asn	Gly	Phe	Arg	
260					265					270						
Ser	Phe	Lys	Arg	Ser	Asp	Pro	Val	Asn	Pro	Tyr	His	Val	Gly	Ser	Gly	
275					280					285						
Tyr	Val	Phe	Ala	Pro	Ala	Thr	Ser	Ala	Asn	Asp	Ser	Glu	Leu	Ser	Ser	
290					295					300						
Asp	Ala	Leu	Thr	Asp	Asp	Ser	Met	Ser	Met	Thr	Asp	Ser	Ser	Val	Asp	
305					310					315					320	
Gly	Val	Pro	Pro	Tyr	Arg	Met	Gly	Ser	Lys	Lys	Gln	Leu	Gln	Arg	Glu	
325					330					335						
Met	His	Arg	Ser	Val	Lys	Ala	Asn	Gly	Gln	Val	Ser	Leu	Pro	His	Phe	
340					345					350						
Pro	Arg	Thr	His	Arg	Leu	Pro	Lys	Glu	Met	Thr	Pro	Val	Glu	Pro	Ala	

355	360	365
Ala Phe Ala Ala Glu Leu Ile Ser Arg Leu Glu Lys Leu Lys Leu Glu		
370	375	380
Leu Glu Ser Arg His Ser Leu Glu Glu Arg Leu Gln Gln Ile Arg Glu		
385	390	395 400
Asp Glu Glu Lys Glu Gly Ser Glu Gln Ala Leu Ser Ser Arg Asp Gly		
405	410	415
Ala Pro Val Gln His Pro Leu Ala Leu Leu Pro Ser Gly Ser Tyr Glu		
420	425	430
Glu Asp Pro Gln Thr Ile Leu Asp Asp His Leu Ser Arg Val Leu Lys		
435	440	445
Thr Pro Gly Cys Gln Ser Pro Gly Val Gly Arg Tyr Ser Pro Arg Ser		
450	455	460
Arg Ser Pro Asp His His His Gln His His His His Gln Gln Cys His		
465	470	475 480
Thr Leu Leu Ser Thr Gly Gly Lys Leu Pro Pro Val Ala Ala Cys Pro		
485	490	495
Leu Leu Gly Gly Lys Ser Phe Leu Thr Lys Gln Thr Thr Lys His Val		
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His His His Tyr Ile His His His Ala Val Pro Lys Thr Lys Glu Glu		
515	520	525
Ile Glu Ala Glu Ala Thr Gln Arg Val Arg Cys Leu Cys Pro Gly Gly		
530	535	540
Thr Asp Tyr Tyr Cys Tyr Ser Lys Cys Lys Ser His Pro Lys Ala Pro		
545	550	555 560
Glu Pro Leu Pro Gly Glu Gln Phe Cys Gly Ser Arg Gly Gly Thr Leu		
565	570	575
Pro Lys Arg Asn Ala Lys Gly Thr Glu Pro Gly Leu Ala Leu Ser Ala		
580	585	590
Arg Asp Gly Gly Met Ser Ser Ala Ala Gly Gly Pro Gln Leu Pro Gly		
595	600	605
Glu Glu Gly Asp Arg Ser Gln Asp Val Trp Gln Trp Met Leu Glu Ser		

610					615					620					
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625					630					635					640
Ser	Tyr	Pro	Leu	Glu	Ser	Ala	Arg	Ala	Ala	Pro	Gly	Glu	Arg	Val	Ser
				645					650					655	
Arg	His	His	Leu	Leu	Gly	Ala	Ser	Gly	His	Ser	Arg	Ser	Val	Ala	Arg
			660					665					670		
Ala	His	Pro	Phe	Thr	Gln	Asp	Pro	Ala	Met	Pro	Pro	Leu	Thr	Pro	Pro
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Asn	Thr	Leu	Ala	Gln	Leu	Glu	Glu	Ala	Cys	Arg	Arg	Leu	Ala	Glu	Val
690						695					700				
Ser	Lys	Pro	Gln	Lys	Gln	Arg	Cys	Cys	Val	Ala	Ser	Gln	Gln	Arg	Asp
705				710					715					720	
Arg	Asn	His	Ser	Ala	Ala	Gly	Gln	Ala	Gly	Ala	Ser	Pro	Phe	Ala	Asn
				725					730					735	
Pro	Ser	Leu	Ala	Pro	Glu	Asp	His	Lys	Glu	Pro	Lys	Lys	Leu	Ala	Ser
			740					745					750		
Val	His	Ala	Leu	Gln	Ala	Ser	Glu	Leu	Val	Val	Thr	Tyr	Phe	Phe	Cys
		755					760					765			
Gly	Glu	Glu	Ile	Pro	Tyr	Arg	Arg	Met	Leu	Lys	Ala	Gln	Ser	Leu	Thr
	770					775					780				
Leu	Gly	His	Phe	Lys	Glu	Gln	Leu	Ser	Lys	Lys	Gly	Asn	Tyr	Arg	Tyr
785				790					795					800	
Tyr	Phe	Lys	Lys	Ala	Ser	Asp	Glu	Phe	Ala	Cys	Gly	Ala	Val	Phe	Glu
			805					810					815		
Glu	Ile	Trp	Asp	Asp	Glu	Thr	Val	Leu	Pro	Met	Tyr	Glu	Gly	Arg	Ile
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<210> 2

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Partial
sequence of conductin protein 78-200 (rgs-domain)

<400> 2

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1 5 10 15

Leu Phe Arg Thr Phe Leu Glu Arg Glu Lys Cys Val Asp Thr Leu Asp
20 25 30

Phe Trp Phe Ala Cys Asn Gly Phe Arg Gln Met Asn Leu Lys Asp Thr
35 40 45

Lys Thr Leu Arg Val Ala Lys Ala Ile Tyr Lys Arg Tyr Ile Glu Asn
50 55 60

Asn Ser Val Val Ser Lys Gln Leu Lys Pro Ala Thr Lys Thr Tyr Ile
65 70 75 80

Arg Asp Gly Ile Lys Lys Gln Gln Ile Gly Ser Val Met Phe Asp Gln
85 90 95

Ala Gln Thr Glu Ile Gln Ala Val Met Glu Glu Asn Ala Tyr Gln Val
100 105 110

Phe Leu Thr Ser Asp Ile Tyr Leu Glu Tyr Val
115 120

<210> 3

<211> 54

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Partial
sequence of conductin protein 343-396 (GSK 3β)

<400> 3

Ala Asn Gly Gln Val Ser Leu Pro His Phe Pro Arg Thr His Arg Leu
1 5 10 15

Pro Lys Glu Met Thr Pro Val Glu Pro Ala Ala Phe Ala Ala Glu Leu

20

25

30

Ile Ser Arg Leu Glu Lys Leu Lys Leu Glu Leu Glu Ser Arg His Ser
 35 40 45

Leu Glu Glu Arg Leu Gln
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<210> 4

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Partial
 sequence of conductin protein 397-465 (β -catenine
 binding domain)

<400> 4

Gln Ile Arg Glu Asp Glu Glu Lys Glu Gly Ser Glu Gln Ala Leu Ser
 1 5 10 15

Ser Arg Asp Gly Ala Pro Val Gln His Pro Leu Ala Leu Leu Pro Ser
 20 25 30

Gly Ser Tyr Glu Glu Asp Pro Gln Thr Ile Leu Asp Asp His Leu Ser
 35 40 45

Arg Val Leu Lys Thr Pro Gly Cys Gln Ser Pro Gly Val Gly Arg Tyr
 50 55 60

Ser Pro Arg Ser Arg
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<210> 5

<211> 51

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Partial
 sequence of conductin protein 783-833 (dishevelled
 homologue region)

<400> 5

Leu Thr Leu Gly His Phe Lys Glu Gln Leu Ser Lys Lys Gly Asn Tyr
1 5 10 15

Arg Tyr Tyr Phe Lys Lys Ala Ser Asp Glu Phe Ala Cys Gly Ala Val
20 25 30

Phe Glu Glu Ile Trp Asp Asp Glu Thr Val Leu Pro Met Tyr Glu Gly
35 40 45

Arg Ile Leu
50

<210> 6

<211> 2825

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA of
conductine protein

<400> 6

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agccgattgc tgagaggaac tggaagaaga aaaaggagga ggagggaaaa aaagcaaaac 180
aaaatccaaa ctcaagtga cgcctcctct caccatgagt agcgcctgtg tagtgactct 240
ccttccagat ccagcagca gcttccgcga ggatgctccg cggcccccg ttccgggaga 300
agaaggggag accccaccgt gtcagcctag tgtgggcaag gtccagtcca ccaaacctat 360
gcccgtttcc tctaattgta ggcggaatga agatggactg ggggagcccg aggggagggc 420
ctccccgat tccccttga ccaggtggac caagtcttta cactccttgt tgggtgacca 480
ggatggtgca tacctcttcc ggactttcct ggagagggag aaatgtgtgg atacgctgga 540
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agtggccaaa gcaatctata agaggtacat tgagaacaac agcgttgtct ccaagcagct 660
gaagcccgcc accaagacct acatacgaga tggcatcaag aagcaacaga tcggctcggg 720
catgtttgac caggcacaga ccgagatcca ggcagtgatg gaggaaaatg cctaccaggt 780
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tgaagaagag gagtggacgt gtgccgacct caagtgcaaa ctctcaccca ccgtgggttg 960
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tgtctttgca ccagccacca gcgccaacga cagcgagtta tccagcgacg cactgaccga 1140
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cagctatgaa gaggaccac aaaccatttt ggacgaccac ctctccaggg tcctcaagac 1560
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ccaccaccag caccaccacc atcagcagtg tcataccctt ctttcgactg ggggcaagct 1680
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cgaggcagaa gccacacaga gagtccgctg cctctgtcct gggggaacag attattattg 1860
ctactccaaa tgcaaaagcc acccgaaggc tccagagccc ctgcctgggg agcagttttg 1920
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gtccaagccc catagtggcc aaagcataag aaagagctac ccattggagt ctgcccgtgc 2160
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aggcaggatc ctgggcaaag tggagaggat cgactgagcc ttggcctcct cggcgtgcaa 2760
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<210> 7

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA partial
sequence 446-814

<400> 7

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aggcagatga acctgaagga taccaaaact ttgcgagtgg ccaaagcaat ctataagagg 180
tacattgaga acaacagcgt tgtctccaag cagctgaagc ccgccacca gacctacata 240
cgagatggca tcaagaagca acagatcggc tcggtcatgt ttgaccaggc acagaccgag 300
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gaatatgtg 369

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<210> 8

<211> 162

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA partial
sequence 1241-1402

<400> 8

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acgcctgtgg aacctgctgc cttegcgcgc gagctcatct ccaggctgga gaaactgaaa 120
ctggagctgg aaagccgcca tagtctggag gagcggctgc ag 162
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<210> 9

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA partial
sequence 1403-1609

<400> 9

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gcaccggtcc agcaccacct ggccctccta ccctccggca gctatgaaga ggaccacaa 120
accattttgg acgaccacct ctccagggtc ctcaagaccc ccggctgtca atcccctggt 180
gtgggtcgct acagcccacg gtcccgc 207
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<210> 10

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA partial
sequence 2561-2713

<400> 10

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aagaaggcga gtgacgaatt tgctgcgga gcagtttttg aggagatctg ggacgacgag 120
acagtgtcc ccatgtacga aggcaggatc ctg 153
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